SEQUENCE LISTING

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      Sebbel, Peter
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<120> Molecular Antigen Array

<130> 1700.0190004

<140> (To be assigned)
<141> 2002-01-18

<150> US 60/262,379
<151> 2001-01-19

<150> US 60/288,549
<151> 2001-05-04

<150> US 60/326,998
<151> 2001-10-05

<150> US 60/331,045
<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

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<400> 1
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<210> 2
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 2
cggtggttac ctgctgcacg cgttgcttaa gcgacatgta gcgg   44

<210> 3
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 3
ccatgaggcc tacgataccc   20

<210> 4
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<220>
<223> Description of Artificial Sequence: Primer

<400> 4
ggcactcacg gcgcgcttta caggc   25

<210> 5
<211> 47
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<220>
<223> Description of Artificial Sequence: Primer

<400> 5
ccttctttaa cggtggttac ctgctggcaa ccaacgtggt tcatgac   47

<210> 6
<211> 40
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 6
aagcatgctg cacgcgtgtg cggtggtcgg atcgcccggc   40

<210> 7
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gggtctagat tcccaaccat tcccttatcc aggctttttg acaacgctat gctccgcgcc 60
catcgtctgc accagctggc ctttgacacc   90

<210> 8
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
gctggtttcg ctaccgtagc gcaggccttc ccaaccattc ccttatcc 108

<210> 9
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<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cccgaattcc tagaagccac agctgccctc c 31

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
cctgcggtgg tctgaccgac accc 24

<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g 41

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ctatcatcta gaatgaatag aggattcttt aac 33

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified ribosome
      binding site

<400> 13
aggaggtaaa aaacg   15

<210> 14
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal peptide

<400> 14
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1   5   10   15

Thr Val Ala Gln Ala
            20

<210> 15
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified Fos
      construct

<400> 15
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
 1   5   10   15

Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
            20   25   30

Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
            35   40   45

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 16
Ala Ala Ala Ser Gly Gly
 1   5

<210> 17
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 17
Gly Gly Ser Ala Ala Ala

1   5

<210> 18
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 18
gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcactggct 60
ggtttcgcta ccgtagcgca ggcctgggtg ggggcggccg cttctggtgg ttgcggtggt 120
ctgaccgaca ccctgcaggc ggaaaccgac caggtggaag acgaaaaatc cgcgctgcaa 180
accgaaatcg cgaacctgct gaaagaaaaa gaaagctgg agttcatcct ggcggcacac 240
ggtggttgct aagctt 256

<210> 19
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 19
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
                5   10   15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
            20   25   30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
        35   40   45

His Gly Gly Cys
    50

<210> 20
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<220>
<221> CDS
<222> (22)..(240)

<400> 20
gaattcagga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg 51
                        Met Lys Lys Thr Ala Ile Ala Ile Ala Val
                         1   5   10

gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
            15   20   25

```
gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg    147
Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
            30                  35                  40

ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag    195
Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
            45                  50                  55

ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct       240
Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
      60                  65                  70
gggtgtgggg atatcaagct t                                            261
```

```
<210> 21
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<400> 21
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
  1               5                  10                  15

Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
            20                  25                  30

Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
            35                  40                  45

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
      50                  55                  60

Gly Gly Cys Gly Gly Ser Ala Ala Ala
  65                  70
```

```
<210> 22
<211> 196
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<220>
<221> CDS
<222> (34)..(189)

<400> 22
gaattcagga ggtaaaaaga tatcgggtgt ggg gcg gcc gct tct ggt ggt tgc    54
                                      Ala Ala Ala Ser Gly Gly Cys
                                        1               5

ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac   102
Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
          10                  15                  20
```

```
gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa    150
Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys
     25                      30                  35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt        196
Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
 40                  45                  50
```

<210> 23
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

```
<400> 23
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
 1               5                  10                  15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
             20                  25                  30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
         35                  40                  45

His Gly Gly Cys
     50
```

<210> 24
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

```
<400> 24
gaattcagga ggtaaaaaac gatggcttgc ggtggtctga ccgacaccct gcaggcggaa 60
accgaccagg tggaagacga aaaatccgcg ctgcaaaccg aaatcgcgaa cctgctgaaa 120
gaaaagaaa agctggagtt catcctggcg gcacacggtg gttgcggtgg ttctgcggcc 180
gctgggtgtg gggatatcaa gctt                                        204
```

<210> 25
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

```
<400> 25
Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
 1               5                  10                  15
Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn
```

```
                20                  25                  30
Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly
         35                  40                  45
Gly Cys Gly Gly Ser Ala Ala Ala
     50                  55
```

<210> 26
<211> 26
<212> PRT
<213> Homo sapiens

<400> 26
```
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1               5                  10                  15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
            20                  25
```

<210> 27
<211> 262
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<400> 27
```
gaattcaggc ctatggctac aggctcccgg acgtccctgc tcctggcttt tggcctgctc 60
tgcctgccct ggcttcaaga gggcagcgct gggtgtgggg cggccgcttc tggtggttgc 120
ggtggtctga ccgacaccct gcaggcggaa accgaccagg tggaagacga aaaatccgcg 180
ctgcaaaccg aaatcgcgaa cctgctgaaa gaaaagaaa agctggagtt catcctggcg 240
gcacacggtg gttgctaagc tt                                       262
```

<210> 28
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<400> 28
```
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
              5                  10                  15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
            20                  25                  30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
         35                  40                  45

His Gly Gly Cys
     50
```

<210> 29

```
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<220>
<221> CDS
<222> (7)..(240)

<400> 29
gaattc atg gct aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc      48
       Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly
       1               5                   10

ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg     96
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu
 15                  20                  25                  30

acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc    144
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser
                35                  40                  45

gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg    192
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
            50                  55                  60

gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct    240
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
        65                  70                  75

gggtgtggga ggcctaagct t                                            261


<210> 30
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<400> 30
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1               5                   10                  15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp
                20                  25                  30

Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu
        35                  40                  45

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
    50                  55                  60

Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
 65                  70                  75
```

<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
cctgggtggg ggcggccgct tctggtggtt gcggtggtct gacc   44

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc   44

<210> 33
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ggtgggaatt caggaggtaa aaaacgatgg cttgcggtgg tctgacc   47

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gcttgcggtg gtctgacc   18

<210> 35
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ccaccaagct tagcaaccac cgtgtgc   27

<210> 36
<211> 54
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
ccaccaagct tgatatcccc acacccagcg gccgcagaac caccgcaacc accg   54

<210> 37
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
ccaccaagct taggcctccc acacccagcg gc   32

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
ggtgggaatt caggaggtaa aaaacgatg   29

<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
ggtgggaatt caggcctatg gctacaggct cc   32

<210> 40
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
ggtgggaatt catggctaca ggctccc   27

<210> 41
<211> 59
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 41
gggtctagaa tggctacagg ctcccggacg tccctgctcc tggctttttgg cctgctctg   59

<210> 42
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
cgcaggcctc ggcactgccc tcttgaagcc agggcaggca gagcaggcca aaagccag   58

<210> 43
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
      venom phospholipase A2

<220>
<221> CDS
<222> (1)..(402)

<400> 43
```
atc atc tac cca ggt act ctg tgg tgt ggt cac ggc aac aaa tct tct    48
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
 1               5                  10                  15

ggt ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc    96
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
            20                  25                  30

acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac    144
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
        35                  40                  45

ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac    192
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
    50                  55                  60

gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct    240
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
 65                 70                  75                  80

tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac    288
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
                85                  90                  95

aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc    336
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
            100                 105                 110

tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg    384
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
            115                 120                 125
```

```
ttc gac ctg cgc aaa tac                                                      402
Phe Asp Leu Arg Lys Tyr
    130
```

<210> 44
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
      venom phospholipase A2

<400> 44
```
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
  1           5              10              15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
            20              25              30

Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
            35              40              45

Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
    50              55              60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
 65              70              75                          80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
                85              90              95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
            100             105             110

Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
            115             120             125

Phe Asp Leu Arg Lys Tyr
    130
```

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
```
ccatcatcta cccaggtac                                                          19
```

<210> 46
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
cccacaccca gcggccgcgt atttgcgcag gtcg   34

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cggtggttct gcggccgcta tcatctaccc aggtac   36

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ttagtatttg cgcaggtcg   19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ccggctccat cggtgcag   18

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
accaccagaa gcggccgcag gggaaacaca tctgcc   36

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51

cggtggttct gcggccgctg gctccatcgg tgcag   35

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
ttaaggggaa acacatctgc c   21

<210> 53
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 53
actagtctag aatgagagtg aaggagaaat atc   33

<210> 54
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 54
tagcatgcta gcaccgaatt tatctaattc caataattct tg   42

<210> 55
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 55
gtagcaccca ccaaggcaaa gctgaaagct acccagctcg agaaactggc a   51

<210> 56
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 56
caaagctcct attcccactg ccagtttctc gagctgggta gctttcag   48

<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
ttcggtgcta gcggtggctg cggtggtctg accgac   36

<210> 58
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
gatgctgggc ccttaaccgc aaccaccgtg tgccgcc   37

<210> 59
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: JUN amino acid
      sequence

<400> 59
Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
 1   5   10   15

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
            20   25   30

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys
        35   40   45

<210> 60
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FOS amino
      acid sequence

<400> 60
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
 1   5   10   15

Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
            20   25   30

Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
        35   40   45

```
<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 61
ccggaattca tgtgcggtgg tcggatcgcc cgg                              33


<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 62
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac                        39


<210> 63
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 63
gttggttgcg gagccgcggg tagcgacatt gacccttata aagaatttgg            50


<210> 64
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgcgtcccaa gcttctacgg aagcgttgat aggatagg                         38


<210> 65
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
ctagccgcgg gttgcggtgg tcggatcgcc cgg                              33


<210> 66
<211> 38
<212> DNA
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 66
cgcgtcccaa gctttagca accaacgtgg ttcatgac   38

<210> 67
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 67
ccggaattca tggacattga cccttataaa g   31

<210> 68
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 68
ccgaccaccg caacccgcgg ctagcggaag cgttgatagg atagg   45

<210> 69
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 69
ctaatggatc cggtgggggc tgcggtggtc ggatcgcccg gctcgag   47

<210> 70
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 70
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac   39

<210> 71
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 71
ccggaattca tggacattga cccttataaa g   31

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 72
ccgaccaccg cagcccccac cggatccatt agtacccacc caggtagc   48

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 73
gttggttgcg gagccgcggg tagcgaccta gtagtcagtt atgtc   45

<210> 74
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 74
cgcgtcccaa gcttctacgg aagcgttgat aggatagg   38

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 75
ctagccgcgg gttgcggtgg tcggatcgcc cgg   33

<210> 76
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 76

cgcgtcccaa gctttttagca accaacgtgg ttcatgac   38

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 77
ccggaattca tggccacact tttaaggagc   30

<210> 78
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 78
cgcgtcccaa gctttttagca accaacgtgg ttcatgac   38

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 79
ccggaattca tggacattga cccttataaa g   31

<210> 80
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 80
cctagagcca cctttgccac catcttctaa attagtaccc acccaggtag c   51

<210> 81
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 81
gaagatggtg gcaaaggtgg ctctagggac ctagtagtca gttatgtc   48

<210> 82
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 82
cgcgtcccaa gcttctaaac aacagtagtc tccggaag   38

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 83
gccgaattcc tagcagctag caccgaattt atctaa   36

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 84
ggttaagtcg acatgagagt gaaggagaaa tat   33

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
taaccgaatt caggaggtaa aaagatatgg   30

<210> 86
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
gaagtaaagc ttttaaccac cgcaaccacc agaag   35

<210> 87
<211> 33
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 87
tcgaatgggc cctcatcttc gtgtgctagt cag   33

<210> 88
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
      construct

<400> 88
Glu Phe Arg Arg
  1

<210> 89
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 89
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
               20   25   30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
           35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
       50   55   60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
 65   70   75   80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
               85   90   95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
               100   105   110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
               115   120   125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
       130   135   140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145   150   155   160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
               165   170   175

Gln Ser Arg Gly Ser Gln Cys

180

<210> 90
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 90
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
                20   25   30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
            35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
        50   55   60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
 65   70   75   80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85   90   95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
                100   105   110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
                115   120   125

Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro
        130   135   140

Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145   150   155   160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165   170   175

Gln Ser Arg Gly Ser Gln Cys
            180

<210> 91
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 91
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
                20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50   55   60

```
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
             85              90              95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115             120             125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130             135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
        180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
        210


<210> 92
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 92
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1              5              10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
             20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
    50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
             85              90              95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130             135             140
```

```
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165                 170                 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180                 185                 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195                 200                 205
Glu Ser Gln Cys
    210


<210> 93
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 93
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1             5                 10                  15

Ser Phe Leu Pro Thr Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
                100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
            180


<210> 94
<211> 212
<212> PRT
<213> Hepatitis B virus
```

<400> 94
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
                85   90   95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
        115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195   200   205

Glu Ser Gln Cys
    210

<210> 95
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 95
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50   55   60

```
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
                85              90              95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130             135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
        180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
        210


<210> 96
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 96
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1              5              10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln
 65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85              90              95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130             135             140
```

```
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165                 170                 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180                 185                 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195                 200                 205
Glu Ser Gln Cys
    210


<210> 97
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 97
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1             5                 10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65                  70                  75                  80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85                  90                  95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100                 105                 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115                 120                 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130                 135                 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165                 170                 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180                 185                 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195                 200                 205

Gly Ser Gln Cys
    210
```

<210> 98
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 98
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20   25   30

Thr Ala Ser Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys
        35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50   55   60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala
65   70   75   80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85   90   95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100   105   110

Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115   120   125

Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130   135   140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145   150   155   160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165   170   175

Gln Ser Arg Glu Ser Gln Cys
            180

<210> 99
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 99
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20   25   30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50   55   60

```
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                     85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
             100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
             115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
     130                 135                 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                 165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
             180
```

```
<210> 100
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 100
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1               5                  10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
             20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
             35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
     50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65                  70                  75                  80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr
                 85                  90                  95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
             100                 105                 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
             115                 120                 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
     130                 135                 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                 165                 170                 175
```

```
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210


<210> 101
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 101
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1               5                   10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
            20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50                  55                  60

Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65                  70                  75                  80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85                  90                  95

Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100                 105                 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115                 120                 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130                 135                 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys
                165                 170                 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210


<210> 102
<211> 183
<212> PRT
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      human Hepatitus B construct

<400> 102
```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
              20                  25                  30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
      50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
              85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
              100                 105                 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
              115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
      130                 135                 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
              165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
              180
```

<210> 103
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 103
```
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1               5                  10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
              20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
          35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
      50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65                  70                  75                  80
```

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser
            85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195   200   205

Glu Ser Gln Cys
    210

<210> 104
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 104
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20   25   30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
            35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50   55   60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65   70   75   80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85   90   95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100   105   110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115   120   125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130   135   140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145   150   155   160

```
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
            165                 170             175

Gln Ser Arg Glu Ser Gln Cys
            180


<210> 105
<211> 183
<212> PRT
<213> Hepatitis B virus
<400> 105
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5               10              15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20              25              30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35              40              45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
    50              55              60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65              70              75              80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85              90              95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100             105             110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115             120             125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130             135             140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145             150             155             160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
            165             170             175

Gln Ser Arg Glu Ser Gln Cys
            180


<210> 106
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 106
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5               10              15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20              25              30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
```

```
                 35                        40                        45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
         50                    55                    60
Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala
65                    70                    75                    80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                 85                    90                    95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
                 100                   105                   110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
                 115                   120                   125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
         130                   135                   140
Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145                   150                   155                   160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                 165                   170                   175
Gln Ser Arg Glu Ser Gln Cys
                 180
```

```
<210> 107
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 107
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1                 5                    10                   15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
                 20                    25                    30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
         35                    40                    45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
         50                    55                    60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65                    70                    75                    80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                 85                    90                    95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
                 100                   105                   110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
                 115                   120                   125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
         130                   135                   140
```

```
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150             155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
        180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210


<210> 108
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 108
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1             5                 10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65             70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
            85              90              95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130             135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
        180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210
```

<210> 109
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 109
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195   200   205

Glu Ser Gln Cys
    210

<210> 110
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 110
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

```
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50              55              60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His
65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
            85              90              95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130             135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195             200             205

Glu Ser Gln Cys
    210
```

```
<210> 111
<211> 212
<212> PRT
<213> Hepatitis B virus


<220>
<221> UNSURE
<222> (28)
<223> May be any amino acid.

<400> 111
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1               5               10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
            20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65              70              75              80
```

```
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
              85                      90                  95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
              100                 105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
          115                 120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
      130                 135             140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150             155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
              165                 170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
              180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg
          195             200             205

Glu Ser Gln Cys
      210


<210> 112
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 112
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1             5                 10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
              20              25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
          35              40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
      50              55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65              70                  75                  80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
              85                  90                  95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
              100                 105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
          115                 120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
      130                 135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150             155                 160
```

```
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195             200             205

Glu Ser Gln Cys
    210


<210> 113
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 113
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1           5               10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85              90              95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100             105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115             120             125

Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val
            130             135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
            165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195             200             205

Glu Ser Gln Cys
    210


<210> 114
```

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 114
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195   200   205

Glu Pro Gln Cys
    210

<210> 115
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 115
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
            85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195   200   205

Glu Ser Gln Cys
    210

<210> 116
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 116
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
            85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr
              165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
          180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
          195   200   205

Glu Ser Gln Cys
    210

<210> 117
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 117
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
          20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
          35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
              85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
              100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln
          115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
              165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
          180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
          195   200   205

Glu Ser Gln Cys
    210

<210> 118
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 118
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
          20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
       35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
    50   55   60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
         85   90   95

Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp
        100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
       115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130   135   140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
        165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
       180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
       195   200   205

Glu Ser Gln Cys
    210

<210> 119
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 119
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu
  1   5   10   15

```
Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp
            20              25                      30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35              40                  45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr
65                  70                  75                      80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                      95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115                 120                 125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
            165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
            180
```

```
<210> 120
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 120
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5                   10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20              25                      30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35              40                  45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65                  70                  75                      80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                      95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115                 120                 125
```

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130   135   140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145   150   155   160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
          165   170   175

Gln Ser Arg Glu Ser Gln Cys
         180

<210> 121
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 121
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
          20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
      35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr
          85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
          100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
          115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
          130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
          165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
          180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
          195   200   205

Glu Ser Gln Cys
      210

<210> 122

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 122
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35   40   45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50   55   60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val
        130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195   200   205

Glu Ser Gln Cys
    210

<210> 123
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 123
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20   25   30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
            35   40   45

```
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val
65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
                100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
            130                 135                 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
                165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
                180


<210> 124
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 124
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
    1               5                   10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
                20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65                  70                  75                  80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn
                85                  90                  95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
                100                 105                 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln
            115                 120                 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
            130                 135                 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160
```

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
              165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
              180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
              195   200   205

Glu Ser Gln Cys
    210

<210> 125
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 125
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
    1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
              20   25   30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
              35   40   45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
       50   55   60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65   70   75   80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
              85   90   95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
              100   105   110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
       115   120   125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130   135   140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145   150   155   160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
              165   170   175

Gln Ser Arg Glu Ser Gln Cys
              180

<210> 126
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 126
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

```
1                5                   10                  15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser
    50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65                  70                  75                  80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
            85                  90                  95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100                 105                 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
            115                 120                 125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130                 135                 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165                 170                 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180                 185                 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            195                 200                 205

Glu Ser Gln Cys
    210


<210> 127
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 127
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
    1               5                   10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35                  40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
    50                  55                  60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65                  70                  75                  80
```

```
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
                85                    90                    95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp
            100                 105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
        115                 120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130                 135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210


<210> 128
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 128
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
  1                 5                  10                  15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
                20                  25                  30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
            35              40                  45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
        50                  55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65                  70                  75          .           80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr
                85                    90                    95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100                 105             110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
        115                 120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
        130                 135             140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145                 150                 155                 160
```

```
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Thr Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210
```

<210> 129
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 129

```
Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr
  1           5               10              15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
            20              25              30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
        35              40              45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
    50              55              60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65              70              75              80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
                85              90              95

Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp
            100             105             110

Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln
        115             120             125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
    130             135             140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145             150             155             160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
                165             170             175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
            180             185             190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
        195             200             205

Glu Ser Gln Cys
    210
```

<210> 130

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 130
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1   5   10   15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
              20   25   30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
          35   40   45

Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
      50   55   60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65   70   75   80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
                  85   90   95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
              100   105   110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
          115   120   125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
      130   135   140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145   150   155   160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
              165   170   175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
              180   185   190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
          195   200   205

Glu Ser Gln Cys
      210

<210> 131
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 131
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1   5   10   15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
              20   25   30

Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35   40   45

```
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65                  70                  75                  80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
            165                 170                 175

Gln Ser Arg Glu Ser Gln Cys
            180
```

```
<210> 132
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 132
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65                  70                  75                  80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145                 150                 155                 160
```

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
           165   170   175

Gln Ser Arg Gly Ser Gln Cys
         180

<210> 133
<211> 3221
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1901)..(2458)

<400> 133
ttccactgcc ttccaccaag ctctgcagga ccccagagtc aggggtctgt attttcctgc 60

tggtggctcc agttcaggaa cagtaaaccc tgctccgaat attgcctctc acatctcgtc 120

aatctccgcg aggactgggg accctgtgac gaacatggag aacatcacat caggattcct 180

aggacccctg ctcgtgttac aggcggggtt tttattgttg acaagaatcc tcacaatacc 240

gcagagtcta gactcgtggt ggacttctct caattttata gggggatcac ccgtgtgtct 300

tggccaaaat tcgcagtccc caacctccaa tcactcacca acctcctgtc tccaatttg 360

tcctggttat cgctggatgt gtctgcggcg ttttatcata ttcctcttca tcctgctgct 420

atgcctcatc ttcttattgg ttcttctgga ttatcaaggt atgttgcccg tttgtcctct 480

aattccagga tcaacaacaa ccagtacggg accatgcaaa acctgcacga ctcctgctca 540

aggcaactct atgtttccct catgttgctg tacaaaacct acggttggaa attgcacctg 600

tattcccatc ccatcgtcct gggctttcgc aaaataccta tgggagtggg cctcagtccg 660

tttctcttgg ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttcccccac 720

tgtttggctt tcagctatat ggatgatgtg gtattggggg ccaagtctgt acagcatcgt 780

gagtcccttt ataccgctgt taccaatttt cttttgtctc tgggtataca tttaaaccct 840

aacaaaacaa aaagatgggg ttattcccta aacttcatgg gttacataat ggaagttgg 900

ggaacattgc acaggatca tattgtacaa aagatcaaac actgttttag aaaacttcct 960

gttaacaggc ctattgattg gaaagtatgt caaagaattg tgggtctttt gggctttgct 1020

gctccattta cacaatgtgg atatcctgcc ttaatgcctt tgtatgcatg tatacaggct 1080

aaacaggctt tcacttctc gccaacttac aaggcctttc taagtaaaca gtacatgaac 1140

ctttacccg ttgctcggca acggcctggt ctgtgccaag tgtttgctga cgcaaccccc 1200

actggttggg gcttggccat aggccatcag cgcatgagtg gaacctttgt ggctcctctg 1260

ccgatccata ctgcggaact cctagccgct tgtattgctc gcagccggtc tggagcaaag 1320

ctcatcggaa ctgacaattc tgtcgtcctc tcgcggaaat atacatcgtt ccatggctg 1380

```
ctaggctgta ctgccaactg gatccttcgc gggacgtcct ttgtttacgt cccgtcggcg   1440

ctgaatcccg cggacgaccc ctctcggggc cgcttgggac tctatcgtcc ccttctccgt   1500

ctgccgttcc agccgaccac ggggcgcacc tctctttacg cggtctcccc gtctgtgcct   1560

tctcatctgc cggtccgtgt gcacttcgct tcacctctgc acgttgcatg gagaccaccg   1620

tgaacgccca tcagatcctg cccaaggtct tacataagag gactcttgga ctcccagcaa   1680

tgtcaacgac cgaccttgag gcctacttca aagactgtgt gtttaaggac tgggaggagc   1740

tgggggagga gattaggtta aaggtctttg tattaggagg ctgtaggcat aaattggtct   1800

gcgcaccagc accatgcaac ttttcacct ctgcctaatc atctcttgta catgtcccac   1860

tgttcaagcc tccaagctgt gccttgggtg gctttggggc atg gac att gac cct   1915
                                             Met Asp Ile Asp Pro
                                              1               5

tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct   1963
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
             10              15              20

gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg   2011
Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
         25              30              35

tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act   2059
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
         40              45              50

gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct   2107
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
     55              60              65

acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta   2155
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
 70              75              80              85

gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg   2203
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu
             90              95             100

tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa   2251
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu
            105             110             115

tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga   2299
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg
            120             125             130

cca cca aat gcc cct atc tta tca aca ctt ccg gaa act act gtt gtt   2347
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val
            135             140             145

aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tcg cct   2395
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
150             155             160             165

cgc aga cgc aga tct caa tcg ccg cgt cgc aga aga tct caa tct cgg   2443
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
            170             175             180
```

```
gaa tct caa tgt tag tattccttgg actcataagg tgggaaactt tactgggctt   2498
Glu Ser Gln Cys
            185

tattcctcta cagtacctat ctttaatcct gaatggcaaa ctccttcctt tcctaagatt   2558

catttacaag aggacattat tgataggtgt caacaatttg tgggccctct cactgtaaat   2618

gaaaagagaa gattgaaatt aattatgcct gctagattct atcctaccca cactaaatat   2678

ttgcccttag acaaaggaat taaaccttat tatccagatc aggtagttaa tcattacttc   2738
caaaccagac attatttaca tactctttgg aaggctggta ttctatataa gagggaaacc   2798

acacgtagcg catcattttg cgggtcacca tattcttggg aacaagagct acagcatggg   2858

aggttggtca ttaaaacctc gcaaaggcat ggggacgaat ctttctgttc ccaaccctct   2918

gggattcttt cccgatcatc agttggaccc tgcattcgga gccaactcaa acaatccaga   2978

ttgggacttc aaccccatca aggaccactg gccagcagcc aaccaggtag gagtgggagc   3038

attcgggcca gggctcaccc ctccacacgg cggtatttg gggtggagcc ctcaggctca   3098

gggcatattg accacagtgt caacaattcc tcctcctgcc tccaccaatc ggcagtcagg   3158

aaggcagcct actcccatct ctccacctct aagagacagt catcctcagg ccatgcagtg   3218

gaa                                                                 3221
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<210> 134
<211> 185
<212> PRT
<213> Hepatitis B virus

<400> 134
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1               5                   10                  15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
            20                  25                  30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
        35                  40                  45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
    50                  55                  60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65                  70                  75                  80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
                85                  90                  95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
            100                 105                 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
        115                 120                 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130                 135                 140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145                 150                 155                 160
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
            165                 170                 175
Arg Ser Gln Ser Arg Glu Ser Gln Cys
        180                 185
```

<210> 135
<211> 188
<212> PRT
<213> Woodchuck hepatitis B virus

<400> 135
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
 1   5   10   15

Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp
            20   25   30
Thr Ala Thr Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys
        35   40   45

Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu
    50   55   60

Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln
65   70   75   80

Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys
                85   90   95

Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln
            100   105   110

His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115   120   125

Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
    130   135   140

Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser
145   150   155   160

Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro
                165   170   175

Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys
                180   185

<210> 136
<211> 217
<212> PRT
<213> Ground squirrel hepatitis virus

<400> 136
Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro
 1   5   10   15

Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp
            20   25   30

Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe
        35   40   45

Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala
    50   55   60

Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro
65   70   75   80

```
His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr
                 85                  90                  95

Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg
                100                 105                 110

Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln
            115                 120                 125

Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val
    130                 135                 140
Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
145                 150                 155                 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
                165                 170                 175

Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg
                180                 185                 190

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
            195                 200                 205

Arg Ser Gln Ser Pro Ala Ser Asn Cys
    210                 215
```

```
<210> 137
<211> 262
<212> PRT
<213> Snow Goose Hepatitis B Virus

<400> 137
Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
  1               5                  10                  15

Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp
                 20                  25                  30

Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
            35                  40                  45

Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr
    50                  55                  60

Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro
65                  70                  75                  80

Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
                 85                  90                  95

Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
                100                 105                 110

Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
            115                 120                 125

Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg
    130                 135                 140

Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr
145                 150                 155                 160
```

Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
             165   170   175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro
          180   185   190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys
       195   200   205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val
   210   215   220
Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro
225   230   235   240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg
          245   250   255

Ser Pro Ser Pro Arg Lys
         260

<210> 138
<211> 305
<212> PRT
<213> Duck hepatitis B virus

<400> 138
Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln
  1   5   10   15

Gly Ile Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu
          20   25   30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala
       35   40   45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro
    50   55   60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr
65   70   75   80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe
          85   90   95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu
          100   105   110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val
       115   120   125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu
   130   135   140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro
145   150   155   160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala
          165   170   175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp
          180   185   190

His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile
    195   200   205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys
    210   215   220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln
225   230   235   240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu
          245   250   255

Pro Arg Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg
          260   265   270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser
     275   280   285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg
    290   295   300

Glu
305

<210> 139
<211> 212
<212> PRT
<213> Haemophilus influenzae

<400> 139
Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
  1   5   10   15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe
          20   25   30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu
      35   40   45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln
    50   55   60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys
65   70   75   80

Asn Val Thr Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val
             85   90   95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu
          100   105   110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val
      115   120   125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val
     130   135   140

Gly Lys Thr Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly
145   150   155   160

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu
          165   170   175

Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala
          180   185   190

Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln
          195   200   205 .

Ile Ala Tyr Glu
    210

<210> 140
<211> 139
<212> PRT
<213> Pseudomonas stutzeri

<400> 140
Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
 1   5   10   15

Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
        20   25   30

Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile
        35   40   45

Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr
    50   55   60

Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
65   70   75   80

Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile
        85   90   95

Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
        100   105   110

Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
        115   120   125

Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser
        130   135

<210> 141
<211> 59
<212> PRT
<213> Caulobacter crescentus

<400> 141
Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr
 1   5   10   15

Ala Ile Glu Tyr Gly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val
        20   25   30

Thr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys
        35   40   45

Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr
        50   55

<210> 142
<211> 173
<212> PRT
<213> Escherichia coli

<400> 142
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
 1   5   10   15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
                20   25   30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
            35   40   45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
        50   55   60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65   70   75   ‹   80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
                85   90   95

Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
                100   105   110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
            115   120   125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
        130   135   140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145   150   155   160

Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
                165   170

<210> 143
<211> 173
<212> PRT
<213> Escherichia coli

<400> 143
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
 1   5   10   15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
                20   25   30

Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
            35   40   45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
        50   55   60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65   70   75   80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
                85   90   95

```
Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
            100                 105                 110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
            115                 120                 125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
    130                 135                 140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145                 150                 155                 160
Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
                165                 170
```

<210> 144
<211> 172
<212> PRT
<213> Escherichia coli

<400> 144
```
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln
  1               5                  10                  15

Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
            20                  25                  30

Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
            35                  40                  45

Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu
    50                  55                  60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn
 65                  70                  75                  80

Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser
                85                  90                  95

Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile
            100                 105                 110

Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly
            115                 120                 125

Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr
    130                 135                 140

Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala
145                 150                 155                 160

Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln
                165                 170
```

<210> 145
<211> 853
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (281)..(829)

<400> 145

```
acgtttctgt ggctcgacgc atcttcctca ttcttctctc caaaaaccac ctcatgcaat 60

ataaacatct ataaataaag ataacaaata gaatattaag ccaacaaata aactgaaaaa 120

gtttgtccgc gatgctttac ctctatgagt caaaatggcc ccaatgtttc atcttttggg 180

ggaaactgtg cagtgttggc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc 240

ccatgtcgat ttagaaatag tttttttgaaa ggaaagcagc atg aaa att aaa act     295
                                              Met Lys Ile Lys Thr
                                               1                  5

ctg gca atc gtt gtt ctg tcg gct ctg tcc ctc agt tct acg acg gct   343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Ser Thr Thr Ala
                    10                  15                  20

ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg   391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
                25                  30                  35

gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa   439
Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
            40                  45                  50

acc gtt cag tta gga cag gtt cgt acc gca tcg ctg gca cag gaa gga   487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
    55                  60                  65

gca acc agt tct gct gtc ggt ttt aac att cag ctg aat gat tgc gat   535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70                  75                  80                  85

acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att   583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
                90                  95                  100

gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt   631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
            105                 110                 115

agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg   679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
            120                 125                 130

ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac   727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
            135                 140                 145

gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc   775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150                 155                 160                 165

gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat   823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
                170                 175                 180

caa taa cctacctagg ttcagggacg ttca                                853
Gln
```

<210> 146
<211> 182
<212> PRT

<213> Escherichia coli

<400> 146
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1   5   10   15
Ser Ser Thr Thr Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
            20   25   30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
        35   40   45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
    50   55   60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65   70   75   80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
                85   90   95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
            100   105   110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
        115   120   125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
    130   135   140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145   150   155   160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
                165   170   175
Phe Lys Val Gln Tyr Gln
            180

<210> 147
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG peptide

<400> 147
Cys Gly Gly Asp Tyr Lys Asp Asp Asp Lys
1   5   10

<210> 148
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 148
ccggaattca tggacattga cccttataaa g   31

<210> 149
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 149
gtgcagtatg gtgaggtgag gaatgctcag gagactc   37

<210> 150
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 150
gsgtctcctg agcattcctc acctcaccat actgcac   37

<210> 151
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 151
cttccaaaag tgagggaaga aatgtgaaac cac   33

<210> 152
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 152
cgcgtcccaa gcttctaaac aacagtagtc tccggaagcg ttgatag   47

<210> 153
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 153
gtggtttcac atttcttccc tcacttttgg aag   33

<210> 154
<211> 281
<212> PRT
<213> Saccharomyces cerevisiae

<400> 154
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
1   5   10   15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
            20   25   30

Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
          35   40   45

Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
      50   55   60

Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
  65   70   75   80

Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
              85   90   95

Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
          100   105   110

Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
          115   120   125

Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
          130   135   140

Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
145   150   155   160

Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
              165   170   175

Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
          180   185   190

Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
          195   200   205

Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser
      210   215   220

Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
225   230   235   240

Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
              245   250   255

Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
          260   265   270

Arg Leu Lys Lys Leu Val Gly Glu Arg
          275   280

<210> 155
<211> 181
<212> PRT
<213> Escherichia coli

<400> 155
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
  1   5   10   15

Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
          20   25   30

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
          35   40   45

```
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
    50              55              60
```

```
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65              70              75              80
```

```
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
                85              90              95
```

```
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
            100             105             110
```

```
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
        115             120             125
```

```
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
    130             135             140
```

```
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145             150             155             160
```

```
Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe
                165             170             175
```

```
Lys Val Gln Tyr Gln
            180
```

```
<210> 156
<211> 447
<212> DNA
<213> Hepatitis B

<220>
<221> CDS
<222> (1)..(447)

<400> 156
atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc    48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1               5              10              15

tcg ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat    96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
             20              25              30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt   144
Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
         35              40              45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac   192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
     50              55              60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca   240
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
 65              70              75              80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag   288
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
                 85              90              95

ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga   336
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
```

```
                  100                    105                         110
gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act    384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115             120                 125

cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg    432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
            130             135                 140

gag act act gtt gtt                                                447
Glu Thr Thr Val Val
145
```

<210> 157
<211> 149
<212> PRT
<213> Hepatitis B

<400> 157

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
                20              25                  30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
            35              40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
        50              55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
 65             70                  75                      80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
                85              90                  95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
                100             105                 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
            115             120                 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
            130             135                 140

Glu Thr Thr Val Val
145
```

<210> 158
<211> 152
<212> PRT
<213> Hepatitis B

<400> 158

```
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1               5                  10                  15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
```

```
                20                      25                      30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
            35                  40                  45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
        50                  55                  60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Gly Gly
65                  70                  75                      80

Lys Gly Gly Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val
                85                  90                  95

Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr
            100                 105                 110

Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp
            115                 120                 125

Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser
        130                 135                 140

Thr Leu Pro Glu Thr Thr Val Val
145                 150


<210>    159
<211>    132
<212>    PRT
<213>    Bacteriophage Q Beta

<400>    159
Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
1                5                   10                  15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
                20                  25                  30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
            35                  40                  45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
        50                  55                  60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65                  70                  75                      80

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
                85                  90                  95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
            100                 105                 110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
            115                 120                 125

Asn Pro Ala Tyr
        130


<210>    160
<211>    129
<212>    PRT
```

<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1   5   10   15

Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
            20   25   30

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
        35   40   45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
    50   55   60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65   70   75   80

Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
                85   90   95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
            100   105   110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
            115   120   125

Tyr

<210> 161
<211> 130
<212> PRT
<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1   5   10   15

Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
            20   25   30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
        35   40   45

Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
    50   55   60

Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65   70   75   80

Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
                85   90   95

Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
            100   105   110

Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
            115   120   125

Ile Tyr
    130

<210> 162
<211> 130
<212> PRT
<213> Bacteriophage GA

<400> 162

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1   5   10   15

Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
            20   25   30

Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
        35   40   45

Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
    50   55   60

Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65   70   75   80

Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
                85   90   95

Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
            100   105   110

Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
        115   120   125

Tyr Ala
    130

<210> 163
<211> 132
<212> PRT
<213> Bacteriophage SP

<400> 163

Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1   5   10   15

Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
            20   25   30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35   40   45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
    50   55   60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
                85   90   95

Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
        115   120   125

Asn Pro Ala Tyr
    130

<210>   164
<211>   130
<212>   PRT
<213>   Bacteriophage MS2

<400>   164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1   5   10   15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
            20   25   30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
        35   40   45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
    50   55   60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65   70   75   80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
            85   90   95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
            100   105   110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
        115   120   125

Ile Tyr
    130

<210>   165
<211>   133
<212>   PRT
<213>   Bacteriophage M11

<400>   165
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1   5   10   15

Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
            20   25   30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35   40   45

```
Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
    50              55              60
```

```
Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65              70              75              80
```

```
Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
            85              90              95
```

```
Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
            100             105             110
```
```
Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
        115             120             125
```

```
Leu Asn Pro Ala Tyr
    130
```


```
<210>   166
<211>   133
<212>   PRT
<213>   Bacteriophage MX1
```

```
<400>   166
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
1               5               10              15
```

```
Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
            20              25              30
```

```
Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35              40              45
```

```
Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
    50              55              60
```

```
Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65              70              75              80
```

```
Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
            85              90              95
```

```
Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
            100             105             110
```

```
Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
        115             120             125
```

```
Leu Asn Pro Ala Tyr
    130
```


```
<210>   167
<211>   330
<212>   PRT
<213>   Bacteriophage NL95
```

```
<400>   167
Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1               5               10              15
```

```
Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
```

                20   25   30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35   40   45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
    50   55   60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Lys Asp Ala Cys
65   70   75   80

Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe
                85   90   95

Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu
            100   105   110

Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu
        115   120   125

Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly
    130   135   140

Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro
145   150   155   160

Gly Gly Thr Gly Thr Tyr Arg Cys Pro Phe Ala Cys Tyr Arg Arg Gly
            165   170   175

Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys
            180   185   190

Gly Ser Glu Ala Leu Val Glu Phe Glu Tyr Ala Leu Glu Asp Phe Leu
        195   200   205

Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp
    210   215   220

Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp
225   230   235   240

Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp
            245   250   255

Val Val Lys Met Gln Pro Pro Gly Thr Phe Asp Ser Pro Arg Tyr Tyr
        260   265   270

Leu His Leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu Val Thr Ala
    275   280   285

Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser
    290   295   300

Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro
305   310   315   320

Val Gln Thr Val Ile Val Ile Pro Ser Leu
            325   330

<210> 168
<211> 134
<212> PRT

<213> Apis mellifera

<400> 168
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1   5   10   15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
            20   25   30

Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
        35   40   45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
    50   55   60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65   70   75   80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
                85   90   95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
            100   105   110

Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
        115   120   125

Phe Asp Leu Arg Lys Tyr
        130

<210> 169
<211> 129
<212> PRT
<213> Apis mellifera

<400> 169
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1   5   10   15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
            20   25   30

Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His
        35   40   45

Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu
    50   55   60

Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys
65   70   75   80

Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro
                85   90   95

Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr
            100   105   110

Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys
        115   120   125

Tyr

<210> 170
<211> 134
<212> PRT
<213> Apis dorsata

<400> 170
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1   5   10   15

Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg
            20   25   30
Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
        35   40   45

Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
    50   55   60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser
65   70   75   80

Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr
                85   90   95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg
            100   105   110

Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
        115   120   125

Phe Asp Leu Arg Lys Tyr
        130

<210> 171
<211> 134
<212> PRT
<213> Apis cerana

<400> 171
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1   5   10   15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
            20   25   30

Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
        35   40   45

Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
    50   55   60

Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser
65   70   75   80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
                85   90   95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
            100   105   110

Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
        115   120   125

Phe Asp Leu Arg Lys Tyr
    130

<210> 172
<211> 136
<212> PRT
<213> Bombus pennsylvanicus

<400> 172

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly Asn Gly Asn Ile Ala Asn
1   5   10   15

Gly Thr Asn Glu Leu Gly Leu Trp Lys Glu Thr Asp Ala Cys Cys Arg
            20   25   30

Thr His Asp Met Cys Pro Asp Ile Ile Glu Ala His Gly Ser Lys His
            35   40   45

Gly Leu Thr Asn Pro Ala Asp Tyr Thr Arg Leu Asn Cys Glu Cys Asp
    50   55   60

Glu Glu Phe Arg His Cys Leu His Asn Ser Gly Asp Ala Val Ser Ala
65   70   75   80

Ala Phe Val Gly Arg Thr Tyr Phe Thr Ile Leu Gly Thr Gln Cys Phe
                85   90   95

Arg Leu Asp Tyr Pro Ile Val Lys Cys Lys Val Lys Ser Thr Ile Leu
            100   105   110

Arg Glu Cys Lys Glu Tyr Glu Phe Asp Thr Asn Ala Pro Gln Lys Tyr
            115   120   125

Gln Trp Phe Asp Val Leu Ser Tyr
    130   135

<210> 173
<211> 142
<212> PRT
<213> Heloderma suspectum

<400> 173
Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1   5   10   15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
            20   25   30

Cys Arg Asp His Asp His Cys Ser Asp Thr Met Ala Ala Leu Glu Tyr
            35   40   45

Lys His Gly Met Arg Asn Tyr Arg Pro His Thr Val Ser His Cys Asp
    50   55   60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Asn Val Lys Asp Arg Thr
65   70   75   80

Ala Asp Leu Val Gly Met Thr Tyr Phe Thr Val Leu Lys Ile Ser Cys
                85   90   95

```
Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Asn Asn Phe Ser Gln
            100             105             110
```

```
Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala
        115             120             125
```

```
Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
    130             135             140
```

```
<210>   174
<211>   143
<212>   PRT
<213>   Heloderma suspectum
```

```
<400>   174
Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1               5               10              15
```

```
Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
            20              25              30
```

```
Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
        35              40              45
```

```
Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
    50              55              60
```

```
Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
65              70              75              80
```

```
Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
            85              90              95
```

```
Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
            100             105             110
```

```
Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
        115             120             125
```

```
Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg
    130             135             140
```

```
<210>   175
<211>   142
<212>   PRT
<213>   Heloderma suspectum
```

```
<400>   175
Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1               5               10              15
```

```
Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
            20              25              30
```

```
Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
        35              40              45
```

```
Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
    50              55              60
```

```
Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
```

```
     65                    70                    75                    80
Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
                    85                  90                  95

Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
            100                 105                 110

Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
            115                 120                 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
    130                 135                 140
```

<210> 176
<211> 574
<212> PRT
<213> IgE heavy chain

<400> 176

```
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1                   5                   10                  15

His Ser Gln Thr Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro
            20                  25                  30

Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile
            35                  40                  45

Asp Ser Tyr Ile His Trp Ile Arg Gln Ala Pro Gly His Gly Leu Glu
        50                  55                  60

Trp Val Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Pro
65                  70                  75                  80

Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp Ala Ser Phe Ser Thr
                85                  90                  95

Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Asp Asp Ser Ala Val Phe
            100                 105                 110

Tyr Cys Ala Lys Ser Asp Pro Phe Trp Ser Asp Tyr Tyr Asn Phe Asp
            115                 120                 125

Tyr Ser Tyr Thr Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
    130                 135                 140

Ser Ser Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys
145                 150                 155                 160

Cys Lys Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu
                165                 170                 175

Ala Thr Gly Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly
            180                 185                 190

Ser Leu Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu
            195                 200                 205

Ser Gly His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp
    210                 215                 220
```

```
Ala Lys Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr
225                 230                 235                 240

Asp Trp Val Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr
                245                 250                 255

Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His
            260                 265                 270

Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro
        275                 280                 285

Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val
    290                 295                 300

Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr
305                 310                 315                 320

Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr
                325                 330                 335

Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr
            340                 345                 350

Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser
        355                 360                 365

Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr
    370                 375                 380

Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr
385                 390                 395                 400

Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu
                405                 410                 415

Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val
            420                 425                 430

Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr
        435                 440                 445

His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
    450                 455                 460

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
465                 470                 475                 480

Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe
                485                 490                 495

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
            500                 505                 510

Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
        515                 520                 525

Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
    530                 535                 540

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
545                 550                 555                 560
```

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
                565   570

<210> 177

<400> 177
000

<210> 178
<211> 13
<212> PRT
<213> IgE Peptides

<400> 178
Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1   5   10

<210> 179
<211> 8
<212> PRT
<213> IgE Mimotype

<400> 179
Ile Asn His Arg Gly Tyr Trp Val
1   5

<210> 180
<211> 8
<212> PRT
<213> IgE Mimotype

<400> 180
Arg Asn His Arg Gly Tyr Trp Val
1   5

<210> 181
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 181

Arg Ser Arg Ser Gly Gly Tyr Trp Leu Trp
1   5   10

<210> 182
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 182
Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1   5   10

<210> 183
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 183
Val Asn Leu Pro Trp Ser Arg Ala Ser Gly
1   5   10

<210> 184
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 184
Val Asn Leu Thr Trp Ser Phe Gly Leu Glu
1   5   10

<210> 185
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 185
Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
1   5   10

<210> 186
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 186
Val Asn Arg Pro Trp Ser Phe Gly Leu Glu
1   5   10

<210> 187
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 187
Val Lys Leu Pro Trp Arg Phe Tyr Gln Val
1   5   10

<210> 188
<211> 10
<212> PRT
<213> IgE Mimotype

<400> 188

Val Trp Thr Ala Cys Gly Tyr Gly Arg Met
1   5   10

<210> 189
<211> 7

<212>   PRT
<213>   IgE Mimotype

<400>   189
Gly Thr Val Ser Thr Leu Ser
1   5

<210>   190
<211>   7
<212>   PRT
<213>   IgE Mimotype

<400>   190
Leu Leu Asp Ser Arg Tyr Trp
1   5

<210>   191
<211>   7
<212>   PRT
<213>   IgE Mimotype

<400>   191
Gln Pro Ala His Ser Leu Gly
1   5

<210>   192
<211>   7
<212>   PRT
<213>   IgE Mimotype

<400>   192
Leu Trp Gly Met Gln Gly Arg
1   5

<210>   193
<211>   15
<212>   PRT
<213>   IgE Mimotype

<400>   193
Leu Thr Leu Ser His Pro His Trp Val Leu Asn His Phe Val Ser
1   5   10   15

<210>   194
<211>   9
<212>   PRT
<213>   IgE Mimotype

<400>   194
Ser Met Gly Pro Asp Gln Thr Leu Arg
1   5

<210>   195
<211>   6
<212>   PRT
<213>   IgE Mimotype

<400> 195
Val Asn Leu Thr Trp Ser
1   5

<210> 196
<211> 56
<212> DNA
<213> Oligonucleotide Primer

<400> 196
tagatgatta cgccaagctt ataatagaaa tagttttttg aaaggaaagc agcatg   56

<210> 197
<211> 45
<212> DNA
<213> Oligonucleotide Primer

<400> 197
gtcaaaggcc ttgtcgacgt tattccatta cgcccgtcat tttgg   45

<210> 198

<211> 4623

<212> DNA

<213> pFIMAIC

<400> 198
agacgaaagg gcctcgtgat acgcctattt ttataggtta atgtcatgat aataatggtt   60

tcttagacgt caggtggcac ttttcgggga aatgtgcgcg gaacccctat ttgtttattt   120

ttctaaatac attcaaatat gtatccgctc atgagacaat aaccctgata aatgcttcaa   180

taatattgaa aaaggaagag tatgagtatt caacatttcc gtgtcgccct tattcccttt   240

tttgcggcat tttgccttcc tgttttgct cacccagaaa cgctggtgaa agtaaaagat   300

gctgaagatc agttgggtgc acgagtgggt tacatcgaac tggatctcaa cagcggtaag   360

atccttgaga gttttcgccc cgaagaacgt tttccaatga tgagcacttt taaagttctg   420

ctatgtggcg cggtattatc ccgtattgac gccgggcaag agcaactcgg tcgccgcata   480

cactattctc agaatgactt ggttgagtac tcaccagtca cagaaaagca tcttacggat   540

ggcatgacag taagagaatt atgcagtgct gccataacca tgagtgataa cactgcggcc   600

aacttacttc tgacaacgat cggaggaccg aaggagctaa ccgcttttt gcacaacatg   660

ggggatcatg taactcgcct tgatcgttgg gaaccggagc tgaatgaagc cataccaaac   720

gacgagcgtg acaccacgat gcctgtagca atggcaacaa cgttgcgcaa actattaact   780

ggcgaactac ttactctagc ttcccggcaa caattaatag actggatgga ggcggataaa   840

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gttgcaggac cacttctgcg ctcggccctt ccggctggct ggtttattgc tgataaatct    900

ggagccggtg agcgtgggtc tcgcggtatc attgcagcac tggggccaga tggtaagccc    960

tcccgtatcg tagttatcta cacgacgggg agtcaggcaa ctatggatga acgaaataga   1020

cagatcgctg agataggtgc ctcactgatt aagcattggt aactgtcaga ccaagtttac   1080

tcatatatac tttagattga tttaaaactt catttttaat ttaaaggat ctaggtgaag   1140

atcctttttg ataatctcat gaccaaaatc ccttaacgtg agttttcgtt ccactgagcg   1200
tcagaccccg tagaaaagat caaaggatct tcttgagatc ctttttttct gcgcgtaatc   1260

tgctgcttgc aaacaaaaaa accaccgcta ccagcggtgg tttgtttgcc ggatcaagag   1320

ctaccaactc ttttccgaa ggtaactggc ttcagcagag cgcagatacc aaatactgtc   1380

cttctagtgt agccgtagtt aggccaccac ttcaagaact ctgtagcacc gcctacatac   1440

ctcgctctgc taatcctgtt accagtggct gctgccagtg cgataagtc gtgtcttacc   1500

gggttggact caagacgata gttaccggat aaggcgcagc ggtcgggctg aacggggggt   1560

tcgtgcacac agcccagctt ggagcgaacg acctacaccg aactgagata cctacagcgt   1620

gagctatgag aaagcgccac gcttcccgaa gggagaaagg cggacaggta ccggtaagc   1680

ggcagggtcg aacaggaga gcgcacgagg gagcttccag ggggaaacgc ctggtatctt   1740

tatagtcctg tcgggtttcg ccacctctga cttgagcgtc gattttgtg atgctcgtca   1800

ggggggcgga gcctatggaa aaacgccagc aacgcggcct ttttacggtt cctggccttt   1860

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ataaatgatt atggcgcact tacccccaaa atgacgggcg taatggaata acgcaggggg    4200

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gctgacccac aataataagc cgctgccgtt tggggcgatg gtgacatcag agagtagcca    6720

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ggcgaatggc gcctgatgcg gtattttctc cttacgcatc tgtgcggtat ttcacaccgc    8280

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ccgccaacac ccgctgacgc gccctgacgg gcttgtctgc tcccggcatc cgcttacaga    8400

caagctgtga ccgtctccgg gagctgcatg tgtcagaggt tttcaccgtc atcaccgaaa    8460
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<211> 13
<212> PRT
<213> Ce3epitope

<400> 207
Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1   5   10

<210> 208
<211> 13
<212> PRT
<213> Ce3mimotope

<400> 208
Cys Gly Gly Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
1   5   10

<210> 209
<211> 9
<212> PRT
<213> Bee venom phospholipase A2 cloning vector

<400> 209
Ala Ala Ala Ser Gly Gly Cys Gly Gly
1   5

<210> 210
<211> 145
<212> PRT
<213> PLA$_2$ fusion protein

<400> 210
Met Ala Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys
1   5   10   15

Ser Ser Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys
                20   25   30

Cys Arg Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser
            35   40   45

Lys His Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp
        50   55   60

Cys Asp Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile
65   70   75   80

Ser Ser Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys
                85   90   95

Cys Tyr Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu
                100   105   110

Gly Arg Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr
            115   120   125

Gln Trp Phe Asp Leu Arg Lys Tyr Ala Ala Ala Ser Gly Gly Cys Gly
        130   135   140

Gly
145

<210>   211
<211>   17
<212>   PRT
<213>   Ce4mimotope

<400>   211
Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1   5   10   15

Ala

<210>   212
<211>   27
<212>   PRT
<213>   Synthetic M2 Peptide

<400>   212
Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys
1   5   10   15

Arg Cys Asn Gly Ser Ser Asp Gly Gly Gly Cys
            20   25

<210>   213
<211>   97
<212>   PRT
<213>   Matrix protein M2

<400>   213
Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1   5   10   15

Cys Arg Cys Asn Gly Ser Ser Asp Pro Leu Ala Ile Ala Ala Asn Ile
            20   25   30

Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe
            35   40   45

Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
    50   55   60

Thr Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65   70   75   80

Gln Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
                85   90   95

Glu

<210>   214

<211>   42

<212>   DNA

<213>   Oligonucleotide

<400>   214
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<210>   215

<211>   129
<212>   PRT

<213>   Bacteriophage f2

<400>   215

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1   5   10   15

Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
            20   25   30

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
        35   40   45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
    50   55   60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65   70   75   80

Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala
                85   90   95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
            100   105   110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
        115   120   125

Tyr

<210>   216

<211>   17

<212>   PRT

<213>   Circular Mimotope

<400>   216

Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1   5   10   15

Ala

<210> 217

<211> 329

<212> PRT

<213> Bacteriophage Q-beta

<400> 217

Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
1   5   10   15

Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
            20   25   30

Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
        35   40   45

Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
    50   55   60

Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
65   70   75   80

Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
                85   90   95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
                100   105   110

Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
            115   120   125

Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Gly Ser Gly
            130   135   140

Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro
145   150   155   160

Gly Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu
                165   170   175

Val Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala
            180   185   190

Val Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu
            195   200   205

Gly Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr
            210   215   220

Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr
225   230   235   240

Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu
            245   250   255

Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu
            260   265   270

Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
    275   280   285

Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
    290   295   300

Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
305   310   315   320

Gln Ala Val Ile Val Val Pro Arg Ala
          325

<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1   5   10   15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
       20   25   30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
       35   40   45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
     50   55   60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
            85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
         100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
       115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
     130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
            165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
        180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
       195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210   215   220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260   265   270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275   280   285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290   295   300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305   310   315   320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325   330   335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340   345   350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355   360   365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370   375   380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385   390   395   400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405   410   415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420   425   430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435   440   445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450   455   460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465   470   475   480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485   490   495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500   505   510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515   520   525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530   535   540

```
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545                 550             555                     560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
            565             570                 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
            580             585                 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
        595             600                 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
    610             615             620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625             630             635                     640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
            645             650             655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
            660             665                 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
        675             680             685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
    690             695             700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705             710             715                     720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
            725             730             735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
            740             745             750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
            755             760             765

Gln Asn
    770
```

<210> 219

<211> 82

<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

```
Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys
1               5               10              15

Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
        20              25              30
```

```
Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
        35              40              45
Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile
    50              55              60
Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val
65              70              75                      80
Val Glu
```

<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

```
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1           5               10                      15
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
        20              25              30
Gly Leu Met Val Gly Gly Val Val Ile Ala
        35              40
```

221:

RANKL_human: TrEMBL:O14788: extracellular domain

```
YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRIK QAFQGAVQKE
LQHIVGSQHI RAEKAMVDGS WLDLAKRSKL EAQPFAHLTI NATDIPSGSH KVSLSSWYHD
RGWAKISNMT FSNGKLIVNQ DGFYYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP
SSHTLMKGGS TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNPSLLD PDQDATYFGA FKVRDID
```


222:

RANKL_human: spliced isoformTrEMBL:O14788

```
MDPNRISEDG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRIKQAF QGAVQKELQH
IVGSQHIRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYHDRGW
AKISNMTFSN GKLIVNQDGF YYLYANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH
TLMKGGSTKY WSGNSEFHFY SINVGGFFKL RSGEEISIEV SNPSLLDPDQ DATYFGAFKV
RDID
```


223:

RANKL_mouse: TrEMBL:O35235: extracellular domain

```
YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESEDT LPDSCRRMKQ AFQGAVQKEL
QHIVGPQRFS GAPAMMEGSW LDVAQRGKPE AQPFAHLTIN AASIPSGSHK VTLSSWYHDR
```

```
GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHHETSGSV PTDYLQLMVY VVKTSIKIPS
SHNLMKGGST KNWSGNSEFH FYSINVGGFF KLRAGEEISI QVSNPSLLDP DQDATYFGAF KVQDID
```

224:

RANKL_mouse spliced isoforms: TrEMBL:Q9JJK8

```
MKQAFQGAVQ KELQHIVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPFAHL TINAASIPSG
SHKVTLSSWY HDRGWAKISN MTLSNGKLRV NQDGFYYLYA NICFRHHETS GSVPTDYLQL
MVYVVKTSIK IPSSHNLMKG GSTKNWSGNS EFHFYSINVG GFFKLRAGEE ISIQVSNPSL
LDPDQDATYF GAFKVQDID
```

225:

MIF_rat: SwissProt
```
PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYYD MNAANVGWNG STFA
```

226:

MIF_mouse: SwissProt
```
PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYYD MNAANVGWNG STFA
```

227:

MIF_human: SwissProt
```
PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFA
```

228:
Human IL-17

```
ACCESSION #:   AAC50341

  1 mtpgktslvs llllllsleai vkagitiprn pgcpnsedkn fprtvmvnln ihnrntntnp
 61 krssdyynrs tspwnlhrne dperypsviw eakcrhlgci nadgnvdyhm nsvpiqqeil
121 vlrrepphcp nsfrlekilv svgctcvtpi vhhva
```

229:
Mouse IL-17

```
        ACCESSION #:   AAA37490

  1 mspgrassvs lmlllllsla atvkaaaiip qssacpntea kdflqnvkvn lkvfnslgak
 61 vssrrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsvliqq
121 eilvlkrepe scpftfrvek mlvgvgctcv asivrqaa
```

230:
Human IL-13 (precursor)

MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG
CSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

231:
Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA
GMYCAALESL INVSGCSAIE KTQRMLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL
HLKKLFREGR FN

232:
Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCNAIYRTQRILHGLCNR
KAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

233:
Human IL-5 (precursor)

MRMLLHLSLL ALGAAYVYAI PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFLGVMNTEW
IIES

234:
Human IL-5 (processed)

I PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ
EFLGVMNTEW IIES

235:
Mouse IL-5 (processed)

MEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGGTVEMLFQNLSLIKK
YIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

236:
CCL21 Swissprot: SY21_human: Sequence after cleavage of signal peptide:
SDGGAQD CCLKYSQRKI PAKVVRSYRK QEPSLGCSIP AILFLPRKRS QAELCADPKE LWVQQLMQHL
DKTPSPQKPA QGCRKDRGAS KTGKKGKGSK GCKRTERSQT PKGP

237:
CCL21 Swissprot: SY21_mouse: Sequence after cleavage of signal peptide:
SDGGGQD CCLKYSQKKI PYSIVRGYRK QEPSLGCPIP AILFSPRKHS KPELCANPEE GWVQNLMRRL

DQPPAPGKQS PGCRKNRGTS KSGKKGKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1_human: Sequence after cleavage of signal peptide:
DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR FKM

239:

Swissprot: SDF1_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNK

240:

BLC Sequences: Human: Accession: NP_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNGC
PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KCRCSGVIST VVGLNIIDRI QVTPPGNGCP
KTEVVIWTKM KKVICVNPRA KWLQRLLRHV QSKSLSSTPQ APVSKRRAA

242:
Human Eotaxin-1
1-23 is Signal peptide
1 mkvsaallwl lliaaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk
61 avifktklak dicadpkkkw vqdsmkyldq ksptpkp

243:
Human Eotaxin-2
1-26 is Signal peptide
1 maglmtivts llflgvcahh iiptgsvvip spccmffvsk ripenrvvsy qlssrstclk
61 agvifttkkg qqfcgdpkqe wvqrymknld akqkkaspra ravavkgpvq rypgnqttc

244:

Human Eotaxin-3

1-23 is signal peptide

```
1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnscsqr
61 avifttkrgk kvcthprkkw vqkyisllkt pkql
```

245:

Mouse Eotaxin-1

1-23 is signal peptide

```
1 mqsstallfl lltvtsftsq vlahpgsipt sccfimtskk ipntllksyk ritnnrctlk
61 aivfktrlgk eicadpkkkw vqdatkhldq klqtpkp
```

246:

Mouse Eotaxin-2

1-25 is signal peptide

```
1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsy qlangsicpk
61 agvifitkkg hkictdpkll wvqrhiqkld akknqpskga kavrtkfavq rrrgnstev
```

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 –185, corresponding to the soluble form of the receptor. Accession: NP_000748

```
MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRLK
SCFTKDYEEH DKACVRTFYE TPLQLLEKVK NVFNETKNLL DKDWNIFSKN CNNSFAECSS
QDVVTKPDCN CLYPKAIPSS DPASVSPHQP LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG
TNWVPEEASG EASEIPVPQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPPEP GSPRISSPRP QGLSNPSTLS
AQPQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTH
ERQSEGSSSP QLQESVFHLL VPSVILVLLA VGGLLFYRWR RRSHQEPQRA DSPLEQPEGS
PLTQDDRQVE LPV
```

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession. NP_031804

```
MTARGAAGRC PSSTWLGSRL LLVCLLMSRS IAKEVSEHCS HMIGNGHLKV LQQLIDSQME
TSCQIAFEFV DQEQLDDPVC YLKKAFFLVQ DIIDETMRFK DNTPNANATE RLQELSNNLN
SCFTKDYEEQ NKACVRTFHE TPLQLLEKIK NFFNETKNLL EKDWNIFTKN CNNSFAKCSS
RDVVTKPDCN CLYPKATPSS DPASASPHQP PAPSMAPLAG LAWDDSQRTE GSSLLPSELP
LRIEDPGSAK QRPPRSTCQT LESTEQPNHG DRLTEDSQPH PSAGGPVPGV EDILESSLGT
NWVLEEASGE ASEGFLTQEA KFSPSTPVGG SIQAETDRPR ALSASPFPKS TEDQKPVDIT
```

DRPLTEVNPM RPIGQTQNNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL
LLPKSHSWGI VLPLGELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS IPLTDTGHVE
QHEGSSDPQI PESVFHLLVP GIILVLLTVG GLLFYKWKWR SHRDPQTLDS SVGRPEDSSL
TQDEDRQVEL PV

249:
Sequence of Human Resistin: Precursor.

MKALCLLLLPVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDLATCPRGFAVTGCTCG
SACGSWDVRAETTCHCQCAGMDWTGARCCRVQP

250:
Sequence of Mouse Resistin: Precursor.

MKNLSFPLLFLFFLVPELLGSSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSC
GSACGSWDIREEKVCHCQCARIDWTAARCCKLQVAS

251:
Lymphotoxin-β:
Swissprot: TNFC_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQGLG FQKLPEEEPE TDLSPGLPAA HLIGAPLKGQ GLGWETTKEQ
AFLTSGTQFS DAEGLALPQD GLYYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLLE
GAETVTPVLD PARRQGYGPL WYTSVGFGGL VQLRRGERVY VN

252:
Lymphotoxin-β:
Swissprot: TNFC_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP
VAQSSREASA WMTILSPAAD STPDPGVQQL PKGEPETDLN PELPAAHLIG AWMSGQGLSW
EASQEEAFLR SGAQFSPTHG LALPQDGVYY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR
AGGAYGRGSP ELLLEGAETV TPVVDPIGYG SLWYTSVGFG GLAQLRSGER VYVNISHPDM
VDYRRGKTFF GAVMVG

253:
RNA-phage PP7:

msktivlsvg eatrtlteiq stadrqifee kvgplvgrlr ltaslrqnga ktayrvnlkl
dqadvvdcst svcgelpkvr ytqvwshdvt ivansteasr kslydltksl vatsqvedlv
vnlvplgr

254:
RNA-phage SP A1 protein:

aklnqvtls kigkngdqtl tltprgvnpt ngvaslseag avpalekrvt vsvaqpsrnr
knfkvqiklq nptactrdac dpsvtrsafa dvtlsftsys tdeeralirt elaalladpl
ivdaidnlnp aywaallvas sgggdnpsdp dvpvvpdvkp pdgtgrykcp facyrlgsiy
evgkegspdi yergdevsvt fdyaledflg ntnwrnwdqr lsdydianrr rcrgngyidl
datamqsddf vlsgrygvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmvigfw
tdskspqlpt dftqfnsanc pvqtviiips l

255:
"Qβ 240":

AKLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

256:
"Qβ 243":

AKLETVTLGKIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

257:
"Qβ 250":

ARLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

258:
"Qβ 259":
ARLETVTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

259:
"Qβ 251":
AKLETVTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

260:
PH19 (SEQ ID NO:260)

TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTCC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTTCATTTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGCGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTCGTCATCCTTGTAGTCGTCCCCACATCCACCCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCGACCTTCGATCCCACATCCACCCCCTCCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTTGTTTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTTAAACAAACAAAGCTAGCACCTCGAGCCCAGCTGCTGGATCCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGTCGTCATCGTCCCCACATCCACCCCCTCCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACTCCTGCTATGGGT

275:

PH42 (SEQ ID NO:275)

GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCAGTGGAACCTGGAACCCAGAGCA

278:

SU7 (SEQ ID NO:278)

AGCTTGCGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:
Resistin-C-Xa:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCCKLQVASSLAGGGGCGIEGR

281:
Resistin-C-EK

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCCKLQVASSLAGGGGCGDDDD

282:
Resistin-GCG:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCCKLQVASSLAGGGGCG

283:

pCep-Xa-Fc*: (complete sequence)

```
   1 GCCCCGCCGC CGGACGAACT AAACCTGACT ACGGCATCTC TGCCCCTTCT TCGCTGGTAC GAGGAGCGCT
  71 TTTGTTTTGT ATTCGGGGCA GTGCATGTAA TCCCTTCAGT TGGTTGGTAC AACTTGCCAA CTGGGCCCTG
 141 TTCCACATGT GACACGGGGG GGGACCAAAC ACAAAGGGGT TCTCTGACTG TAGTTGACAT CCTTATAAAT
 211 GGATGTGCAC ATTTGCCAAC ACTGAGTGGC TTTCATCCTG GAGCAGACTT TGCATGCTGT GGACTGCAAC
 281 ACAACATTGC CTTTATGTGT AACTCTTGGC TGAAGCTCTT ACACCAATGC TGGGGGACAT GTACCTCCCA
 351 GGGGCCCAGG AAGACTACGG GAGGCTACAC CAACGTCAAT CAGAGGGGCC TGTGTAGCTA CCGATAAGCG
 421 GACCCTCAAG AGGGCATTAG CAATAGTGTT TATAAGGCCC CCTTGTTAAC CCTAAACGGG TAGCATATGC
 491 TTCCCGGGTA GTAGTATATA CTATCCAGAC TAACCCTAAT TCAATAGCAT ATGTTACCCA ACGGGAAGCA
 561 TATGCTATCG AATTAGGGTT AGTAAAAGGG TCCTAAGGAA CAGCGATATC TCCCACCCCA TGAGCTGTCA
 631 CGGTTTTATT TACATGGGGT CAGGATTCCA CGAGGGTAGT GAACCATTTT AGTCACAAGG GCAGTGGCTG
 701 AAGATCAAGG AGCGGGCAGT GAACTCTCCT GAATCTTCGC CTGCTTCTTC ATTCTCCTTC GTTTAGCTAA
 771 TAGAATAACT GCTGAGTTGT GAACAGTAAG GTGTATGTGA GGTGCTCGAA AACAAGGTTT CAGGTGACGC
 841 CCCCAGAATA AAATTTGGAC GGGGGGGTTCA GTGGTGGCAT TGTGCTATGA CACCAATATA ACCCTCACAA
 911 ACCCCTTGGG CAATAAATAC TAGTGTAGGA ATGAAACATT CTGAATATCT TTAACAATAG AAATCCATGG
 981 GGTGGGGACA AGCCGTAAAG ACTGGATGTC CATCTCACAC GAATTTATGG CTATGGGCAA CACATAATCC
1051 TAGTGCAATA TGATACTGGG GTTATTAAGA TGTGTCCCAG GCAGGGACCA AGACAGGTGA ACCATGTTGT
1121 TACACTCTAT TTGTAACAAG GGGAAAGAGA GTGGACGCCG ACAGCAGCGG ACTCCACTGG TTGTCTCTAA
1191 CACCCCCGAA AATTAAACGG GGCTCCACGC CAATGGGGCC CATAAACAAA GACAAGTGGC CACTCTTTTT
1261 TTTGAAATTG TGGAGTGGGG GCACGCGTCA GCCCCCACAC GCCGCCCTGC GGTTTTGGAC TGTAAAATAA
1331 GGGTGTAATA ACTTGGCTGA TTGTAACCCC GCTAACCACT GCGGTCAAAC CACTTGCCCA CAAAACCACT
1401 AATGGCACCC CGGGGAATAC CTGCATAAGT AGGTGGGCGG GCCAAGATAG GGGCGCGATT GCTGCGATCT
1471 GGAGGACAAA TTACACACAC TTGCGCCTGA GCCCCAAGCA CAGGGTTGTT GGTCCTCATA TTCACGAGGT
1541 CGCTGAGAGC ACGGTGGGCT AATGTTGCCA TGGGTAGCAT ATACTACCCA AATATCTGGA TAGCATATGC
1611 TATCCTAATC TATATCTGGG TAGCATAGGC TATCCTAATC TATATCTGGG TAGCATATGC TATCCTAATC
1681 TATATCTGGG TAGTATATGC TATCCTAATT TATATCTGGG TAGCATAGGC TATCCTAATC TATATCTGGG
1751 TAGCATATGC TATCCTAATC TATATCTGGG TAGTATATGC TATCCTAATC TGTATCCGGG TAGCATATGC
1821 TATCCTAATA GAGATTAGGG TAGTATATGC TATCCTAATT TATATCTGGG TAGCATATAC TACCCAAATA
1891 TCTGGATAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
1961 ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGT ATATGCTATC
2031 CTAATTTATA TCTGGGTAGC ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA
2101 TCTGGGTAGT ATATGCTATC CTAATCTGTA TCCGGGTAGC ATATGCTATC CTCATGCATA TACAGTCAGC
2171 ATATGATACC CAGTAGTAGA GTGGGAGTGC TATCCTTTGC ATATGCCGCC ACCTCCCAAG GGGGCGTGAA
2241 TTTTCGCTGC TTGTCCTTTT CCTGCATGCT GGTTGCTCCC ATTCTTAGGT GAATTTAAGG AGGCCAGGCT
2311 AAAGCCGTCG CATGTCTGAT TGCTCACCAG GTAAATGTCG CTAATGTTTT CCAACGCGAG AAGGTGTTGA
2381 GCGCGGAGCT GAGTGACGTG ACAACATGGG TATGCCCAAT TGCCCCATGT TGGGAGGACG AAAATGGTGA
2451 CAAGACAGAT GGCCAGAAAT ACACCAACAG CACGCATGAT GTCTACTGGG GATTTATTCT TTAGTGCGGG
2521 GGAATACACG GCTTTTAATA CGATTGAGGG CGTCTCCTAA CAAGTTACAT CACTCCTGCC CTTCCTCACC
2591 CTCATCTCCA TCACCTCCTT CATCTCCGTC ATCTCCGTCA TCACCCTCCG CGGCAGCCCC TTCCACCATA
2661 GGTGGAAACC AGGGAGGCAA ATCTACTCCA TCGTCAAAGC TACACACAGT CACCCTGATA TTGCAGGTAG
2731 GAGCGGGCTT TGTCATAACA AGGTCCTTAA TCGCATCCTT CAAAACCTCA GCAAATATAT GAGTTTGTAA
2801 AAAGACCATG AAATAACAGA CAATGGACTC CCTTAGCGGG CCAGGTTGTG GGCCGGGTCC AGGGGCCATT
2871 CCAAAGGGGA GACGACTCAA TGGTGTAAGA CGACATTGTG GAATAGCAAG GGCAGTTCCT CGCCTTAGGT
2941 TGTAAAGGGA GGTCTTACTA CCTCCATATA CGAACACACC GGCGACCCAA GTTCCTTCGT CGGTAGTCCT
3011 TTCTACGTGA CTCCTAGCCA GGGAGAGCTCT TAAACCTTCT GCAATGTTCT CAAATTTCGG GTTGGAACCT
3081 CCTTGACCAC GATGCTTTCC AAACCACCCT CCTTTTTTGC GCCTGCCTCC ATCACCCTGA CCCCGGGGTC
3151 CAGTGCTTGG GCCTTCTCCT GGGTCATCTG CGGGGCCCTG CTCTATCGCT CCCGGGGGCA CGTCAGGCTC
3221 ACCATCTGGG CCACCTTCTT GGTGGTATTC AAAATAATCG GCTTCCCCTA CAGGGTGGAA AAATGGCCTT
3291 CTACCTGGAG GGGGCCTGCG CGGTGGAGAC CCGGATGATG ATGACTGACT ACTGGGACTC CTGGGCCTCT
3361 TTTCTCCACG TCCACGACCT CTCCCCCTGG CTCTTTCACG ACTTCCCCCC CTGGCTCTTT CACGTCCTCT
3431 ACCCCGGCGG CCTCCACTAC CTCCTCGACC CCGGCCTCCA CTACCTCCTC GACCCCGGCC TCCACTGCCT
3501 CCTCGACCCC GGCCTCCACC TCCTGCTCCT GCCCCTCCTG CTCCTGCCCC TCCTGCTGCT CCTGCCCCTC
3571 CTGCCCCTCC TGCTCCTGCC CCTCCTGCCC CTCCTGCTCC TGCCCCTCCT GCCCCTCCTG CTCCTGCCCC
3641 TCCTGCCCCT CCTCCTGCTC CTGCCCCTCC TGCCCCTCCT CCTGCTCCTG CCCCTCCTGC CCCTCCTGCT
3711 CCTGCCCCTC CTGCCCCTCC TGCTCCTGCC CCTCCTGCCC CTCCTGCTCC TGCCCCTCCT GCTCCTGCCC
3781 CTCCTGCTCC TGCCCCTCCT GCTCCTGCCC CTCCTGCCCC TCCTGCCCCT CCTGCTCCTG CTGCCCCTGC
3851 TGCTCCTGCC CCTCCTGCCC CTCCTGCCCC TCCTGCTCCT GCCCCTCCTC CTGCTCCTGC CCCTCCTGCC
3921 CCTCCTGCCC CTCCTCCTGC TCCTGCCCCT CCTGCCCCTC CTCCTGCTCC TGCCCCTCCT CCTGCTCCTG
3991 CCCCTCCTGC CCCTCCTGCC CCTCCTCCTG CTCCTGCCCC TCCTGCCCCT CCTCCTGCTC CTGCCCCTCC
4061 TCCTGCTCCT GCCCCTCCTG CCCCTCCTGC CCTCCTGCTC CTGCCCCTCC TCCTGCTCCT GCTCCTGCCC
4131 CCTGCCCCTC CTGCCCCTCC TGCCCCTCCT CCTGCTCCTG CCCCTCCTCC TGCTCCTGCC CCTCCTGCTC
4201 CTGCCCCTCC CGCTCCTGCT CCTGCTCCTG TTCCACCGTG GGTCCCTTTG CAGCCAATGC AACTTGGACG
4271 TTTTTGGGGT CTCCGGACAC CATCTCTATG TCTTGGCCCT GATCCTGAGC CGCCCGGGGC TCCTGGTCTT
4341 CCGCCTCCTC GTCCTCGTCC TCTTCCCCGT CCTCGTCCAT GGTTATCACC CCCTCTTCTT TGAGGTCCAC
4411 TGCCGCCGGA GCCTTCTGGT CCAGATGTGT CTCCCTTCTC TCCTAGGCCA TTTCCAGGTC CTGTACCTGG
4481 CCCCTCGTCA GACATGATTC ACACTAAAAG AGATCAATAG ACATCTTTAT TAGACGACGC TCAGTGAATA
4551 CAGGGAGTGC AGACTCCTGC CCCCTCCAAC AGCCCCCCCA CCCTCATCCC CTTCATGGTC GCTGTCAGAC
4621 AGATCCAGGT CTGAAAATTC CCCATCCTCC GACCATCCT CGTCCTCATC ACCAATTACT CGCACGCCGG
4691 AAAACTCCCG CTGAACATCC TCAAGATTTG CGTCCTGAGC CTCAAGCCAG GCCTCAAATT CCTCGTCCCC
4761 CTTTTTGCTG GACGGTAGGG ATGGGGATTC TCGGGACCCC TCCTCTTCCT CTTCAAGGTC ACCAGACAGA
4831 GATGCTACTG GGGCAACGGA AGAAAAGCTG GGTGCGGCCT GTGAGGATCA GCTTATCGAT GATAAGCTGT
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 4901  CAAACATGAG AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA
 4971  ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT
 5041  TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA
 5111  AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT
 5181  GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT
 5251  ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
 5321  GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG CCGGGCAAGA GCAACTCGGT
 5391  CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG
 5461  GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT
 5531  GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
 5601  GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA
 5671  TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA
 5741  CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT
 5811  GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT
 5881  CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA
 5951  GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
 6021  TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC
 6091  CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC
 6161  TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG
 6231  GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC
 6301  TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
 6371  AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG
 6441  TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA
 6511  CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC
 6581  GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC
 6651  TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG
 6721  GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGCGCCGC
 6791  GTGCGGCTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT GGTTTGCGCA TTCACAGTTC
 6861  TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA TCCGTTAGCG AGGCCATCCA GCCTCGCGTC
 6931  GAACTAGATG ATCCGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
 7001  GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG
 7071  CAGAAGTATG CAAAGCATGC ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG
 7141  CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT TATGCAGAGG
 7211  CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCT GACCGCCACG
 7281  ACCGGTGCCG CCACCATCCC CTGACCCACG CCCCTGACCC CTCACAAGGA GACGACCTTC CATGACCGAG
 7351  TACAAGCCCA CGGTGCGCCT CGCCACCCGC GACGACGTCC CCCGGGCCGT ACGCACCCTC GCCGCCGCGT
 7421  TCGCCGACTA CCCCGCCACG CGCCACACCG TCGACCCCGA CCGCCACATC GAACGCGTCA CCGAGCTGCA
 7491  AGAACTCTTC CTCACGCGCG TCGGGCTCGA CATCGGCAAG GTGTGGGTCG CGGACGACGG CGCCGCGGTG
 7561  GCGGTCTGGA CCACGCCGGA GAGCGTCGAA GCGGGGGCGG TGTTCGCCGA GATCGGCCCG CGCATGGCCG
 7631  AGTTGAGCGG TTCCCGGCTG GCCGCGCAGC AACAGATGGA AGGCCTCCTG GCGCCGCACC GGCCCAAGGA
 7701  GCCCGCGTGG TTCCTGGCCA CCGTCGGCGT CTCGCCCGAC CACCAGGGCA AGGGTCTGGG CAGCGCCGTC
 7771  GTGCTCCCCG GAGTGGAGGC GGCCGAGCGC GCCGGGGTGC CCGCCTTCCT GGAGACCTCC GCGCCCCGCA
 7841  ACCTCCCCTT CTACGAGCGG CTCGGCTTCA CCGTCACCGC CGACGTCGAG TGCCCGAAGG ACCGCGCGAC
 7911  CTGGTGCATG ACCCGCAAGC CCGGTGCCTG ACGCCCGCCC CACGACCCGC AGCGCCCGAC CGAAAGGAGC
 7981  GCACGACCCG GTCCGACGGC GGCCCACGGG TCCCAGGGGG GTCGACCTCG AAACTTGTTT ATTGCAGCTT
 8051  ATAATGGTTA CAAATAAAGC AATAGCATCA CAAATTTCAC AAATAAAGCA TTTTTTTCAC TGCATTCTAG
 8121  TTGTGGTTTG TCCAAACTCA TCAATGTATC TTATCATGTC TGGATCGATC CGAACCCCTT CCTCGACCAA
 8191  TTCTCATGTT TGACAGCTTA TCATCGCAGA TCCGGGCAAC GTTGTTGCAT TGCTGCAGGC GCAGAACTGG
 8261  TAGGTATGGA AGATCTATAC ATTGAATCAA TATTGGCAAT TAGCCATATT AGTCATTGGT TATATAGCAT
 8331  AAATCAATAT TGGCTATTGG CCATTGCATA CGTTGTATCT ATATCATAAT ATGTACATTT ATATTGGCTC
 8401  ATGTCCAATA TGACCGCCAT GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA
 8471  TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC
 8541  CCAACGACCC CGCCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA
 8611  TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA
 8681  AGTCCGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAC
 8751  GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
 8821  GTACACCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT
 8891  GGGAGTTTGT TTTGGCACCA AAATCAACGG GACTTTCCAA AATGTCGTAA TAACCCCGCC CCGTTGACGC
 8961  AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTGGT TTAGTGAACC GTCAGATCTC
 9031  TAGAAGCTGG GTACCGGGAT CCAGCAGCTG GGCTCGAGGT GCTAGCGGGA GGGGGTGGAT GTGGGATCGA
 9101  AGGTCGCAAG CTTACTCACA CATGCCCACC GTGCCCAGCA CCTGAAGCCG AGGGGGCACC GTCAGTCTTC
 9171  CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA GGTCACATGC GTGGTGGTGG
 9241  ACGTGAGCCA CGAAGACCCT GAGGTCAAGT TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA
 9311  GACAAAGCCG CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT CCTGCACCAG
 9381  GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA ACAAAGCCCT CCCAGCCTCC ATCGAGAAAA
 9451  CCATCTCCAA AGCCAAAGGG CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGATGAGCT
 9521  GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA GCGACATCGC CGTGGAGTGG
 9591  GAGAGCAATG GGCAGCCGGA GAACAACTAC AAGACCACGC CTCCCGTGTT GGACTCCGAC GGCTCCTTCT
 9661  TCCTCTACAG CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT
 9731  GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC TCCCTGTCTC CGGGTAAATG ACTCGAGGCC
 9801  CGAACAAAAA CTCATCTCAG AAGAGGATCT GAATAGCGCC GTCGACCATC ATCATCATCA TCATTGAGTT
 9871  TNAACGATCC AGACATGATA AGATACATTG ATGAGTTTGG ACAAACCACA ACTAGAATGC AGTGAAAAAA
 9941  ATGCTTTATT TGTGAAATTT GTGATGCTAT TGCTTTATTT GTAACCATTA TAAGCTGCAA TAAACAAGTT
10011  AACAACAACA ATTGCATTCA TTTTATGTTT CAGGTTCAGG GGGAGGTGGG GAGGTTTTTT AAAGCAAGTA
10081  AAACCTCTAC AAATGTGGTA TGGCTGATTA TGATCCGGCT GCCTCGCGCG TTTCGGTGAT GACGGTGAAA
10151  ACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC
10221  CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG GTGTCGGGGC GCAGCCATGA CCGGTCGACT CTAGA
```

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

·286:
5'LT• long-*Nhe*I: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:
5'LT• short-*Nhe*I: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:
3'LT• stop-*Not*I: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:
GST-EK-C-LT• 49-306: SEQ ID NO:289

APLVMSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQAQKRLDDSKPSCILPSPSSL
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPEL
PAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARS
LTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMV
DYRRGKTFFGAVMVG

290:
GST-EK-C-LT• 126-306: SEQ ID NO:290

APLVMSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGA
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLTLRSALY
RAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGKT
FFGAVMVG

291:

his-myc-EK-C-LT• $_{49-306}$: SEQ ID NO:291

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ

AQKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDPGV

QQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY

RGRTPPAGRSRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSG

ERVYVNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT• $_{126-306}$: SEQ ID NO:292

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDPGVQQLP

KGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRT

PPAGRSRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVY

VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCC GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'
(SEQ ID NO:295)

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGG TGT G-3'

(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEGGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID
NO:309)

310:

met-human-MIF-C1

```
MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG
```

311:

human-MIF-C1 (SEQ ID NO:311)

```
PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG
```

312:

met-human-MIF-C2 (SEQ ID NO:312)

```
MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKTHTSPPCG
```

313:

human-MIF-C2 (SEQ ID NO:313)

```
PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKTHTSPPCG
```

314:

met-human-MIF-C3 (SEQ ID NO:314)

```
MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA  QNRSYSKLLCGLLAERLRISPDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG
```

315:

human-MIF-C3 (SEQ ID NO:315)

```
PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA  QNRSYSKLLCGLLAERLRISPDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG
```

316:

RANKL-UP:

5'CTGCCAGGGGCCCGGGTGCGGCGGTGGCCATCATCACCACCATCACCAGCGCTTCTCAGGAG-3'

317:

RANKL-DOWN :

5'-CCGCTCGAGTTAGTCTATGTCCTGAACTTTGAAAG-3'

318 and 319:
Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)
cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

```
   1 M   S   P   I   L   G   Y   W   K   I   K   G   L   V   Q   P   T   R   L   L   L   E   Y   L   E
   1 atgtcccctatactaggttattggaaaattaagggccttgtgcaacccactcgacttcttttggaatatcttgaa
  26 E   K   Y   E   E   H   L   Y   E   R   D   E   G   D   K   W   R   N   K   K   F   E   L   G   L
  76 gaaaaatatgaagagcatttgtatgagcgcgatgaaggtgataaatggcgaaacaaaaagtttgaattgggtttg
  51 E   F   P   N   L   P   Y   Y   I   D   G   D   V   K   L   T   Q   S   M   A   I   I   R   Y   I
 151 gagtttcccaatcttccttattatattgatggtgatgttaaattaacacagtctatggccatcatacgttatata
  76 A   D   K   H   N   M   L   G   G   C   P   K   E   R   A   E   I   S   M   L   E   G   A   V   L
 226 gctgacaagcacaacatgttgggtggttgtccaaaagagcgtgcagagatttcaatgcttgaaggagcggttttg
 101 D   I   R   Y   G   V   S   R   I   A   Y   S   K   D   F   E   T   L   K   V   D   F   L   S   K
 301 gatattagatacggtgtttcgagaattgcatatagtaaagactttgaaactctcaaagttgatttcttagcaag
 126 L   P   E   M   L   K   M   F   E   D   R   L   C   H   K   T   Y   L   N   G   D   H   V   T   H
 376 ctacctgaaatgctgaaaatgttcgaagatcgtttatgtcataaaacatatttaaatggtgatcatgtaacccat
 151 P   D   F   M   L   Y   D   A   L   D   V   V   L   Y   M   D   P   M   C   L   D   A   F   P   K
 451 cctgacttcatgttgtatgacgctcttgatgttgttttatacatggacccaatgtgcctggatgcgttcccaaaa
 176 L   V   C   F   K   K   R   I   E   A   I   P   Q   I   D   K   Y   L   K   S   S   K   Y   I   A
 526 ttagtttgttttaaaaaacgtattgaagctatcccacaaattgataagtacttgaaatccagcaagtatatagca
 201 W   P   L   Q   G   W   Q   A   T   F   G   G   G   D   H   P   P   K   S   D   L   E   V   L   F
 601 tggcctttgcagggctggcaagccacgtttggtggtggcgaccatcctccaaaatcggatctggaagttctgttc
 226 Q   G   P   C   C   G   G   H   H   H   H   H   Q   R   F   S   G   A   P   A   M   M   E
 676 cagGGGCCCGGGTGCGGCGGTGGCCATCATCACCACCATCACCAGCGCTTCTCAGGAGCTCCAGCTATGATGGAA
 251 C   S   W   L   D   V   A   Q   R   G   K   P   T   A   H   L   T   I   N   A   A
 751 GGCTCATGGTTGGATGTGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCC
 276 S   T   P   S   G   S   A   K   V   T   L   S   S   W   Y   H   D   R   G   W   A   K   I   S   N
 826 AGCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAAC
 301 M   T   F   S   N   G   K   L   R   V   N   Q   D   G   F   Y   Y   L   Y   A   N   I   C   F   R
 901 ATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTTCGG
 326 H   H   E   T   S   G   S   V   P   T   D   Y   L   Q   L   M   V   V   V   K   I   S   I   K
 976 CATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCGTTAAAACCAGCATCAAA
 351 I   P   S   S   H   N   L   M   K   G   G   S   T   K   N   W   S   G   N   S   I   F   H   F   Y
1051 ATCCCAAGTTCTCATAACCTGATGAAAGGAGGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTAT
 376 S   I   N   V   G   G   F   F   K   L   R   A   G   F   I   L   S   I   Q   V   S   N   P   S   L
1126 TCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCCCTG
 401 L   D   P   D   Q   D   A   T   Y   F   G   A   F   K   V   Q   D   I   D   *
1201 CTGGATCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCAGGACATAGACTAACTCGAGCGG
```

320:

Human-C-RANKL

GCGGGGQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFK
LRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID

321:

Primer 5'PrP-*Bam*HI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-*Nhe*I

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP~t~-EK-Fc*

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDKLTHTCPPCPAPEA
EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
K

324:

mPrP~t~

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
DDDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

mouse C-IL-13-F: (SEQ ID NO:328)

ADPGCGGGGGLAGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCN
AIYRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPFLEVLAIEGR
329:

mouse C-IL-13-S: (SEQ ID NO:329)

LACGGGGGGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCNAI
YRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

330:

human C-IL-13-F: (SEQ ID NO:330)

ADPGCGGGGGLAGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCS
AIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFNLEVLAIEGR

331:

human C-IL-13-S: (SEQ ID NO:331)

LACGGGGGGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR
MLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN
332:

mouse C-IL-5-E: (SEQ ID NO:332)

ALVGCGGPKPSTPPGSSGGAPASMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQG
LDILKNQTVRGGTVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

333:

mouse C-IL-5-F: (SEQ ID NO:333)

ADPGCGGGGGLAMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVR
GGTVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEGLEVLAIEGR

334:
mouse C-IL-5-S: (SEQ ID NO:334)

LACGGGGGMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGG
TVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

335:

human C-IL-5-E: (SEQ ID NO:335)

ALVGCGGPKPSTPPGSSGGAPASIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGI
GTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

336:

human C-IL-5-F: (SEQ ID NO:336)

ADPGCGGGGGLAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQG
GTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGGIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT
VERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:
primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCCGGTGCCAAGATC

339:
primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCCGTGGCGAA

340:
primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGGTTCTTCTGGCGGTGCTCCGGCTAGCATGGAGATTCCCATGAGCAC

341:
Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGCGGCGGCCCGAAACCGAGCACCCCGCCGGGTTCTTC

342:
Primer IL5StopXho-R: (SEQ ID NO:342)

TTTTGCGGCCGCGTTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:
Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATCGCCTCTGTC

344:
Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTTGTGTGAACTCGGAC

345:
mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

PFIAS VSDQHGIVYI TENKNKTVVI PCRGSISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVLNCTA
RTELNVGLDF TWHSPPSKSH HKKIVNRDVK PFPGTVAKMF LSTLTIESVT KSDQGEYTCV
ASSGRMIKRN RTFVRVHTKP

346

human C-LT• 49-306 : (SEQ ID NO:346)

LACGGQDQGRRVEKIIGSGAQAQKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSR
EASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSP
THGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG
YGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT• 126-306 : (SEQ ID NO:347)

LACGGSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGL
ALPQDGVYYLYCHVGYRGRTPPAGRSRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSL
WYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDE
YSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQ
RGRLAGGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQ
YSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDR
YSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG